

## APPENDIX A

US-09-746-491-21  
; Sequence 21, Application US/09746491  
; Patent No. US20020137202A1  
; GENERAL INFORMATION:  
; APPLICANT: Burgess, Catherine E.  
; TITLE OF INVENTION: No. US20020137202A1 Proteins and Nucleic Acids Encoding Same  
; FILE REFERENCE: 15966-621  
; CURRENT APPLICATION NUMBER: US/09/746,491  
; CURRENT FILING DATE: 2000-12-20  
; PRIOR APPLICATION NUMBER: USSN 60/171,329  
; PRIOR FILING DATE: 1999-12-21  
; NUMBER OF SEQ ID NOS: 72  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 21  
; LENGTH: 1216  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-746-491-21

### Alignment Scores:

Pred. No.:	4.05e-127	Length:	1216
Score:	1051.00	Matches:	212
Percent Similarity:	68.39%	Conservative:	0
Best Local Similarity:	68.39%	Mismatches:	0
Query Match:	94.68%	Indels:	98
DB:	9	Gaps:	1

US-10-074-978A-24 (1-212) x US-09-746-491-21 (1-1216)

Qy	1 ValGlyAlaAlaValPheAspAlaLeuGluSerGluAlaGluSerGlyArgGlnArgLeu	20
Db	61 GTGGGCGCTGCTGTCTCGACGCGCTCGAGTCCGAGGCGGAAAGCGGCCAGCGACTG	120
Qy	21 LeuValGlnLysArgGlyAlaLeuArgArgLysPheGlyPheSerAlaGluAspTyrArg	40
Db	121 CTGGTCCAGAACGGGGCGCTCTCCGAGGAAGTTCGGCTTCTCGCCGAGGACTACCGC	180
Qy	41 GluLeuGluArgLeuAlaLeuGlnAlaGluProHisArgAlaGlyArgGlnTrpLysPhe	60
Db	181 GAGCTGGAGCGCCTGGCGCTCCAGGCTGAGCCCCACCGCGCCGCCAGTGGAAAGTTC	240
Qy	61 ProGlySerPheTyrPheAlaIleThrValIleThrIleGluTyrGlyHisAlaAla	80
Db	241 CCCGGCTCTTCACTTCGGCATCACCGTCACTACCACATCGAGTACGGCCACGCCGCG	300
Qy	81 ProGlyThrAspSerGlyLysValPheCysMetPheTyrAlaLeuGlyIleProLeu	100
Db	301 CCCGGTACGGACTCCGCAAGGTCTTCTGATGTTCTACCGCGCTCTGGCATCCCGCTG	360
Qy	101 ThrLeuValThrPheGlnSerLeuGlyGluArgLeuAsnAlaValValArgArgLeuLeu	120
Db	361 ACGCTGGTCACCTTCCAGAGCCTGGCGAACGGCTGAACGCCGGTGGTGCAGCGCTCTG	420
Qy	121 LeuAlaAlaLysCysCysLeuGlyLeuArgTrpThrCysValSerThrGluAsnLeuVal	140
Db	421 TTGGCGGCCAAGTGCTGCCTGGCCCTGGGTGGACGTGCGTGTCCACGGAGAACCTGGTG	480
Qy	141 ValAlaGlyLeuLeuAlaCysAlaAlaThrLeuAlaLeuGlyAlaValAlaPheSerHis	160
Db	481 GTGGCCGGCTGCTGGCGTGTGCCACCCCTGGCCCTGGGGCCGTGCCTCTCGCAC	540
Qy	161 PheGluGlyTrpThrPhePheHisAlaTyrTyrCysPheIleThrLeuThrThrIle	180
Db	541 TTGAGGGCTGGACCTTCTCCACGCCTACTACTGCTTCACTCACCCCTACCACCATC	600
Qy	181 GlyPheGly-----	183

Art Unit: 1652

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Db 601 GGCTTCGGCGACTTCGTGGCACTGCAGAGCGCGAGGCCTGCAGAGGAAGCTCCCTAC 660  
Qy 183 ----- 183  
Db 661 GTGGCCTTCAGCTCCTACATCCTCCTGGGCTACGGTATTGGCGCTTCCTAAC 720  
Qy 183 ----- 183  
Db 721 CTGGTGGTCCCTGCGCTTCCTCGTTGCCAGCGCCGACTGGCCGAGCGCGCTGCCGCACC 780  
Qy 183 ----- 183  
Db 781 CCCAGCCCGCGCCCCCGGGGCGCCCGAGAGCCGTGGCTCTGGCTGCCCGCCGCCG 840  
Qy 183 ----- 183  
Db 841 GCCCGCTCCGTGGCTCCGCTCTGTCTTCTGCCACGTGCACAAGCTGGAGAGGTGCC 900  
Qy 184 ---AspAsnLeuGlyPheSerProProSerSerProGlyValValArgGlyGlyGlnAla 202  
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Db 901 CGCGACAACTGGGCTTTCGCCCCCTCGAGCCCCGGGTCTGCGTGGCGAGGCT 960  
Qy 203 ProArgLeuGlyAlaArgTrpLysSerIle 212  
||| ||| ||| ||| ||| ||| ||| ||| |||  
Db 961 CCCAGGCTTGGGGCCCGTGGAAAGTCCATC 990